



PCT

## RAW SEQUENCE LISTING

DATE: 09/20/2004

PATENT APPLICATION: US/10/506,756

TIME: 13:21:52

Input Set : A:\PCTGB2003001049.seqlist.txt

Output Set: N:\CRF4\09172004\J506756.raw

3 <110> APPLICANT: Sense Proteomic Limited  
 4 Blackburn, Jonathan M  
 5 Kozlowski, Roland Z  
 6 Davies, Andrew  
 7 Godber, Ben  
 8 Hart, Darren  
 10 <120> TITLE OF INVENTION: Arrays and Methods  
 12 <130> FILE REFERENCE: P33676WO  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/506,756  
 C--> 15 <141> CURRENT FILING DATE: 2004-09-08  
 17 <150> PRIOR APPLICATION NUMBER: GB 0205910.3  
 18 <151> PRIOR FILING DATE: 2002-03-13  
 20 <160> NUMBER OF SEQ ID NOS: 6  
 22 <170> SOFTWARE: PatentIn version 3.2  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 334  
 26 <212> TYPE: PRT  
 27 <213> ORGANISM: Homo sapiens  
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 36 20 25 30  
 39 Asp Glu Val Ala Glu Arg Leu Met Thr Ile Ala Tyr Glu Ser Gly Val  
 40 35 40 45  
 43 Asn Leu Phe Asp Thr Ala Glu Val Tyr Ala Ala Gly Lys Ala Glu Val  
 44 50 55 60  
 47 Ile Leu Gly Ser Ile Ile Lys Lys Lys Gly Trp Arg Arg Ser Ser Leu  
 48 65 70 75 80  
 51 Val Ile Thr Thr Lys Leu Tyr Trp Gly Gly Lys Ala Glu Thr Glu Arg  
 52 85 90 95  
 55 Gly Leu Ser Arg Lys His Ile Ile Glu Gly Leu Lys Gly Ser Leu Gln  
 56 100 105 110  
 59 Arg Leu Gln Leu Glu Tyr Val Asp Val Val Phe Ala Asn Arg Pro Asp  
 60 115 120 125  
 63 Ser Asn Thr Pro Met Glu Glu Ile Val Arg Ala Met Thr His Val Ile  
 64 130 135 140  
 67 Asn Gln Gly Met Ala Met Tyr Trp Gly Thr Ser Arg Trp Ser Ala Met  
 68 145 150 155 160  
 71 Glu Ile Met Glu Ala Tyr Ser Val Ala Arg Gln Phe Asn Met Ile Pro  
 72 165 170 175  
 75 Pro Val Cys Glu Gln Ala Glu Tyr His Leu Phe Gln Arg Glu Lys Val  
 76 180 185 190

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79 Glu Val Gln Leu Pro Glu Leu Tyr His Lys Ile Gly Val Gly Ala Met
80      195      200      205
83 Thr Trp Ser Pro Leu Ala Cys Gly Ile Ile Ser Gly Lys Tyr Gly Asn
84      210      215      220
87 Gly Val Pro Glu Ser Ser Arg Ala Ser Leu Lys Cys Tyr Gln Trp Leu
88 225      230      235      240
91 Lys Glu Arg Ile Val Ser Glu Glu Gly Arg Lys Gln Gln Asn Lys Leu
92      245      250      255
95 Lys Asp Leu Ser Pro Ile Ala Glu Arg Leu Gly Cys Thr Leu Pro Gln
96      260      265      270
99 Leu Ala Val Ala Trp Cys Leu Arg Asn Glu Gly Val Ser Ser Val Leu
100     275     280     285
103 Leu Gly Ser Ser Thr Pro Glu Gln Leu Ile Glu Asn Leu Gly Ala Ile
104     290     295     300
107 Gln Val Leu Pro Lys Met Thr Ser His Val Val Asn Glu Ile Asp Asn
108 305     310     315     320
111 Ile Leu Arg Asn Lys Pro Tyr Ser Lys Lys Asp Tyr Arg Ser
112     325     330
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116 <211> LENGTH: 333
117 <212> TYPE: PRT
118 <213> ORGANISM: Homo sapiens
120 <400> SEQUENCE: 2
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126 Cys Leu Gly Leu Gly Thr Trp Val Thr Phe Gly Gly Gln Ile Thr Asp
127      20      25      30
130 Glu Met Ala Glu Gln Leu Met Thr Leu Ala Tyr Asp Asn Gly Ile Asn
131      35      40      45
134 Leu Phe Asp Thr Ala Glu Val Tyr Ala Ala Gly Lys Ala Glu Val Val
135      50      55      60
138 Leu Gly Asn Ile Ile Lys Lys Lys Gly Trp Arg Arg Ser Ser Leu Val
139 65      70      75      80
142 Ile Thr Thr Lys Ile Phe Trp Gly Gly Lys Ala Glu Thr Glu Arg Gly
143      85      90      95
146 Leu Ser Arg Lys His Ile Ile Glu Gly Leu Lys Ala Ser Leu Glu Arg
147      100     105     110
150 Leu Gln Leu Glu Tyr Val Asp Val Val Phe Ala Asn Arg Pro Asp Pro
151      115     120     125
154 Asn Thr Pro Met Glu Glu Thr Val Arg Ala Met Thr His Val Ile Asn
155      130     135     140
158 Gln Gly Met Ala Met Tyr Trp Gly Thr Ser Arg Trp Ser Ser Met Glu
159 145     150     155     160
162 Ile Met Glu Ala Tyr Ser Val Ala Arg Gln Phe Asn Leu Thr Pro Pro
163      165     170     175
166 Ile Cys Glu Gln Ala Glu Tyr His Met Phe Gln Arg Glu Lys Val Glu
167      180     185     190
170 Val Gln Leu Pro Glu Leu Phe His Lys Ile Gly Val Gly Ala Met Thr
171      195     200     205

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174 Trp Ser Pro Leu Ala Cys Gly Ile Val Ser Gly Lys Tyr Asp Ser Gly
175      210      215      220
178 Ile Pro Pro Tyr Ser Arg Ala Ser Leu Lys Gly Tyr Gln Trp Leu Lys
179 225      230      235      240
182 Asp Lys Ile Leu Ser Glu Glu Gly Arg Arg Gln Gln Ala Lys Leu Lys
183      245      250      255
186 Glu Leu Gln Ala Ile Ala Glu Arg Leu Gly Cys Thr Leu Pro Gln Leu
187      260      265      270
190 Ala Ile Ala Trp Cys Leu Arg Asn Glu Gly Val Ser Ser Val Leu Leu
191      275      280      285
194 Gly Ala Ser Asn Ala Asp Gln Leu Met Glu Asn Ile Gly Ala Ile Gln
195      290      295      300
198 Val Leu Pro Lys Leu Ser Ser Ser Ile Ile His Glu Ile Asp Ser Ile
199 305      310      315      320
202 Leu Gly Asn Lys Pro Tyr Ser Lys Lys Asp Tyr Arg Ser
203      325      330
206 <210> SEQ ID NO: 3
207 <211> LENGTH: 330
208 <212> TYPE: PRT
209 <213> ORGANISM: Homo sapiens
211 <400> SEQUENCE: 3
213 Gly Thr Gly Met Lys Tyr Arg Asn Leu Gly Lys Ser Gly Leu Arg Val
214 1      5      10      15
217 Ser Cys Leu Gly Leu Gly Thr Trp Val Thr Phe Gly Ser Gln Ile Ser
218      20      25      30
221 Asp Glu Thr Ala Glu Asp Val Leu Thr Val Ala Tyr Glu His Gly Val
222      35      40      45
225 Asn Leu Phe Asp Thr Ala Glu Val Tyr Ala Ala Gly Lys Ala Glu Arg
226      50      55      60
229 Thr Leu Gly Asn Ile Leu Lys Ser Lys Gly Trp Arg Arg Ser Ser Tyr
230 65      70      75      80
233 Val Ile Thr Thr Lys Ile Phe Trp Gly Gly Gln Ala Glu Thr Glu Arg
234      85      90      95
237 Gly Leu Ser Arg Lys His Ile Ile Glu Gly Leu Arg Gly Ser Leu Glu
238      100      105      110
241 Arg Leu Gln Leu Gly Tyr Val Asp Ile Val Phe Ala Asn Arg Ser Asp
242      115      120      125
245 Pro Asn Cys Pro Met Glu Glu Ile Val Arg Ala Met Thr Tyr Val Ile
246      130      135      140
249 Asn Gln Gly Leu Ala Leu Tyr Trp Gly Thr Ser Arg Trp Gly Ala Ala
250 145      150      155      160
253 Glu Ile Met Glu Ala Tyr Ser Met Ala Arg Gln Phe Asn Leu Ile Pro
254      165      170      175
257 Pro Val Cys Glu Gln Ala Glu His His Leu Phe Gln Arg Glu Lys Val
258      180      185      190
261 Glu Met Gln Leu Pro Glu Leu Tyr His Lys Ile Gly Val Gly Ser Val
262      195      200      205
265 Thr Trp Tyr Pro Leu Ala Cys Gly Leu Ile Thr Ser Lys Tyr Asp Gly
266      210      215      220

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269 Arg Val Pro Asp Thr Cys Arg Ala Ser Ile Lys Gly Tyr Gln Trp Leu
270 225                230                235                240
273 Lys Asp Lys Val Gln Ser Glu Asp Gly Lys Lys Gln Gln Ala Lys Val
274                245                250                255
277 Met Asp Leu Leu Pro Val Ala His Gln Leu Gly Cys Thr Val Ala Gln
278                260                265                270
281 Leu Ala Ile Ala Trp Cys Leu Arg Ser Glu Gly Val Ser Ser Val Leu
282                275                280                285
285 Leu Gly Val Ser Ser Ala Glu Gln Leu Ile Glu His Leu Gly Ala Leu
286                290                295                300
289 Gln Val Leu Ser Gln Leu Thr Pro Gln Thr Val Met Glu Ile Asp Gly
290 305                310                315                320
293 Leu Leu Gly Asn Lys Pro His Ser Lys Lys
294                325                330
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298 <211> LENGTH: 334
299 <212> TYPE: PRT
300 <213> ORGANISM: Rattus sp.
302 <400> SEQUENCE: 4
304 Gly Thr Gly Met Lys Tyr Arg Asn Leu Gly Lys Ser Gly Leu Arg Val
305 1                5                10                15
308 Ser Cys Leu Gly Leu Gly Thr Trp Val Thr Phe Gly Gly Gln Ile Ser
309                20                25                30
312 Asp Glu Val Ala Glu Arg Leu Met Thr Ile Ala Tyr Glu Ser Gly Val
313                35                40                45
316 Asn Leu Phe Asp Thr Ala Glu Val Tyr Ala Ala Gly Lys Ala Glu Val
317                50                55                60
320 Ile Leu Gly Ser Ile Ile Lys Lys Lys Gly Trp Arg Arg Ser Ser Leu
321 65                70                75                80
324 Val Ile Thr Thr Lys Leu Tyr Trp Gly Gly Lys Ala Glu Thr Glu Arg
325                85                90                95
328 Gly Leu Ser Arg Lys His Ile Ile Glu Gly Leu Lys Gly Ser Leu Gln
329                100               105               110
332 Arg Leu Gln Leu Glu Tyr Val Asp Val Val Phe Ala Asn Arg Pro Asp
333                115               120               125
336 Ser Asn Thr Pro Met Glu Glu Ile Val Arg Ala Met Thr His Val Ile
337                130               135               140
340 Asn Gln Gly Met Ala Met Tyr Trp Gly Thr Ser Arg Trp Ser Ala Met
341 145               150               155               160
344 Glu Ile Met Glu Ala Tyr Ser Val Ala Arg Gln Phe Asn Met Ile Pro
345                165               170               175
348 Pro Val Cys Glu Gln Ala Glu Tyr His Leu Phe Gln Arg Glu Lys Val
349                180               185               190
352 Glu Val Gln Leu Pro Glu Leu Tyr His Lys Ile Gly Val Gly Ala Met
353                195               200               205
356 Thr Trp Ser Pro Leu Ala Cys Gly Ile Ile Ser Gly Lys Tyr Gly Asn
357                210               215               220
360 Gly Val Pro Glu Ser Ser Arg Ala Ser Leu Lys Cys Tyr Gln Trp Leu
361 225               230               235               240

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364 Lys Glu Arg Ile Val Ser Glu Glu Gly Arg Lys Gln Gln Asn Lys Leu
365                245                250                255
368 Lys Asp Leu Ser Pro Ile Ala Glu Arg Leu Gly Cys Thr Leu Pro Gln
369                260                265                270
372 Leu Ala Val Ala Trp Cys Leu Arg Asn Glu Gly Val Ser Ser Val Leu
373                275                280                285
376 Leu Gly Ser Ser Thr Pro Glu Gln Leu Ile Glu Asn Leu Gly Ala Ile
377                290                295                300
380 Gln Val Leu Pro Lys Met Thr Ser His Val Val Asn Glu Ile Asp Asn
381 305                310                315                320
384 Ile Leu Arg Asn Lys Pro Tyr Ser Lys Lys Asp Tyr Arg Ser
385                325                330
388 <210> SEQ ID NO: 5
389 <211> LENGTH: 333
390 <212> TYPE: PRT
391 <213> ORGANISM: Rattus sp.
393 <400> SEQUENCE: 5
395 Gly Leu Gln Phe Tyr Arg Asn Leu Gly Lys Ser Gly Leu Arg Val Ser
396 1                5                10                15
399 Cys Leu Gly Leu Gly Thr Trp Val Thr Phe Gly Gly Gln Ile Thr Asp
400                20                25                30
403 Glu Met Ala Glu His Leu Met Thr Leu Ala Tyr Asp Asn Gly Ile Asn
404                35                40                45
407 Leu Phe Asp Thr Ala Glu Val Tyr Ala Ala Gly Lys Ala Glu Val Val
408                50                55                60
411 Leu Gly Asn Ile Ile Lys Lys Lys Gly Trp Arg Arg Ser Ser Leu Val
412 65                70                75                80
415 Ile Thr Thr Lys Ile Phe Trp Gly Gly Lys Ala Glu Thr Glu Arg Gly
416                85                90                95
419 Leu Ser Arg Lys His Ile Ile Glu Gly Leu Lys Ala Ser Leu Glu Arg
420                100               105               110
423 Leu Gln Leu Glu Tyr Val Asp Val Phe Ala Asn Arg Pro Asp Pro
424                115               120               125
427 Asn Thr Pro Met Glu Glu Thr Val Arg Ala Met Thr His Val Ile Asn
428                130               135               140
431 Gln Gly Met Ala Met Tyr Trp Gly Thr Ser Arg Trp Ser Ser Met Glu
432 145               150               155               160
435 Ile Met Glu Ala Tyr Ser Val Ala Arg Gln Phe Asn Leu Ile Pro Pro
436                165               170               175
439 Ile Cys Glu Gln Ala Glu Tyr His Met Phe Gln Arg Glu Lys Val Glu
440                180               185               190
443 Val Gln Leu Pro Glu Leu Phe His Lys Ile Gly Val Gly Ala Met Thr
444                195               200               205
447 Trp Ser Pro Leu Ala Cys Gly Ile Val Ser Gly Lys Tyr Asp Ser Gly
448                210               215               220
451 Ile Pro Pro Tyr Ser Arg Ala Ser Leu Lys Gly Tyr Gln Trp Leu Lys
452 225               230               235               240
455 Asp Lys Ile Leu Ser Glu Glu Gly Arg Arg Gln Gln Ala Lys Leu Lys
456                245               250               255

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VERIFICATION SUMMARY

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Input Set : A:\PCTGB2003001049.seqlist.txt

Output Set: N:\CRF4\09172004\J506756.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application Number

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date